

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:58:47 : Search time 75.59 Seconds
(without alignments)
17.633 Million cell updates/sec

Title: US-09-884-696-6
Sequence: 1 FLSELNLEAE 12

Scoring Table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
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7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
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11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
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16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	927	22	AA62110 M. bovis Dalton 2d
2	43	75.4	450	22	AAE04637 Pasteurella haemol
3	43	75.4	608	22	AAE04636 Pasteurella haemol
4	43	75.4	924	12	AA10889 Leukotoxin 352 enc
5	43	75.4	924	14	AA42385 Recombinant leukot
6	43	75.4	924	14	AA42380 Recombinant leukot
7	43	75.4	924	14	AA42378 Recombinant leukot
8	43	75.4	926	12	AA14482 LK352. Pasteurel
9	43	75.4	926	14	AA14482 Leukotoxin 352 pro
10	43	75.4	926	15	AA50291 Recombinant leukot
11	43	75.4	926	17	AAW03945 P. haemolytica tru

12	43	75.4	926	19	AAW9568 Leukotoxin 352 pol
13	43	75.4	936	14	AA34547 GNRH-leukotoxin ge
14	43	75.4	943	14	AA34546 Somatostatin-leuko
15	43	75.4	951	14	AA34548 Rotavirus VP4-leuk
16	43	75.4	953	11	AA07167 105KD PTX protein
17	43	75.4	953	12	AA15159 Leukotoxin from P.
18	43	75.4	953	14	AA43865 Leukotoxin protein
19	43	75.4	953	15	AA60072 PtxA protein of Pa
20	43	75.4	953	22	AAE04638 Pasteurella haemol
21	43	75.4	956	12	AA12561 APPA haemolysin an
22	43	75.4	956	18	AAW22156 ApxII protein. A
23	43	75.4	956	21	AA51410 A. pleuropneumonia
24	43	75.4	977	17	AAW03942 LKT-GNRH protein f
25	43	75.4	977	19	AAW9569 LKT-GNRH chimeric
26	43	75.4	1069	15	AA52748 Bovine IFNgamma/LK
27	43	75.4	1069	18	AA13867 Chimeric protein
28	43	75.4	1069	21	AA21074 Bovine gamma-IPN/p
29	43	75.4	1098	13	AA52747 Bovine IL-2 - LKT
30	43	75.4	1098	15	AA52747 Bovine IL-2/LKT ch
31	43	75.4	1098	18	AA13866 Chimeric protein
32	43	75.4	1098	21	AA21073 Bovine IL-2/Pasteu
33	41	71.9	28	20	AA31518 Extensin agonist pe
34	41	71.9	28	20	AA52482 Extensin agonist pe
35	41	71.9	28	20	AA17577 Extensin agonist pe
36	41	71.9	28	21	AA11144 extensin agonist pe
37	41	71.9	28	21	AA111234 extensin agonist pe
38	41	71.9	28	21	AA52903 Extensin agonist c
39	41	71.9	28	21	AA53000 Extensin agonist c
40	41	71.9	28	21	AA194057 Amino acid sequenc
41	41	71.9	28	21	AA194155 Amino acid sequenc
42	41	71.9	28	22	AAE08396 Extensin agonist pe
43	41	71.9	28	22	AAE08486 Extensin agonist pe
44	41	71.9	28	22	AA64232 Extensin agonist, S
45	41	71.9	28	22	AA64322 Extensin agonist, S

ALIGNMENTS

RESULT 1
AAB62110
ID AAB62110 standard; Protein; 927 AA.
AC AAB62110:
DT 29-MAY-2001 (first entry)
DE M. bovis Dalton 2d RTX toxin A subunit.
KW Moraxella; antigen; immune response; infection; RTX toxin; vaccine;
KW antibacterial; A subunit.
OS Moraxella bovis.
PN WC200116172-A1.
PD 08-MAR-2001.
PF 31-AUG-2000; 2000WO-AU01048.
PR 31-AUG-1999; 99AU-0002571.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (UYME) UNIV MELBOURNE.
XX Farn J, Strugnell R, Tennent J;
XX WPI: 2001-235092/24.
XX N-PSDB; AAF57290.
XX Novel Moraxella bovis antigen useful in compositions for raising immune
XX response in an animal, has protease, lipase or hemolysin activity -

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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:56:22 : Search time 40.83 Seconds
(without alignments)
2181.602 Million cell updates/sec

Title: US-09-884-696-2

Perfect score: 4646

Sequence: 1 MSNTNVIKSNQAGLNSTKMS.....SSNALQPTQIGILAPSV 927

Scoring table: BLAST62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 71.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2325	50.0	953	B30169	leukotoxin A - Pas
2	2240.5	48.2	956	B33389	toxin II - Actinob
3	2236	48.1	955	A35254	leukotoxin A - Pas
4	2209.5	47.6	956	A43834	toxin II - Actinob
5	1959.5	42.2	1052	B49219	toxin III - Actino
6	1928	41.5	1049	S51784	toxin III - Actino
7	1851.5	39.9	1024	S10056	hemolysin A - Esch
8	1849	39.8	1023	L1EECA	hemolysin A - Esch
9	1820	39.2	1055	A37205	leukotoxin A - Act
10	1767.5	38.0	1022	I39643	RTX-toxin I - Acti
11	1752	37.7	998	T00227	hemolysin A toxin
12	1733	37.3	998	T41078	hemolysin - Escher
13	809.5	17.4	1705	S51672	adenylate cyclase
14	806	17.3	1706	CVB8C	cyclolysin - Borde
15	434	9.3	1829	S35027	cytokinin RTX homo
16	432.5	9.3	1829	S35027	iron-regulated pro
17	416	9.0	1302	C81182	iron-regulated pro
18	411	8.8	1208	C82779	hemolysin-type cal
19	410	8.8	1636	B82736	hemolysin-type cal
20	403.5	8.7	1115	A47058	Fe-regulated RTX C
21	391	8.4	2064	G82562	bacteriocin XF2407
22	383	8.2	208	S34238	leukotoxin A - Pas
23	365	7.9	697	F81856	probable RTX-famil
24	343	7.4	4936	AH2515	hypothetical prote
25	332.5	7.2	1944	AH3098	rhicobactin/RTX to
26	328.5	7.2	1990	A56188	probable phosphoes
27	328.5	7.1	1996	C82521	hemolysin-type cal
28	305.5	6.6	993	AE1905	outer membrane sec
29	304.5	6.6	1072	G95851	probable hemolysin

ALIGNMENTS

RESULT 1

B30169 leukotoxin A - Pasteurella haemolytica (serotype 1)

N:Alternate names: lktA protein

C:Species: Pasteurella haemolytica

C>Date: 12-Oct-1989 #sequence: Revision 15-Nov-1996 #ext_change 18-Jun-1999

C:Accession: B30169; C32051; S29516

R:Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstein, G.M.

DNA 8, 15-28, 1989

A:Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.

A:Reference number: A30169; MUID:89210283

A:Accession: B30169

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-953 <HIC>

R:Strathdee, C.A.; Lo, R.Y.C.

J: Bacteriol 171, 916-928, 1989

A:Title: Cloning, nucleotide sequence, and characterization of genes encoding the se

A:Reference number: A32051; MUID:89123172

A:Accession: C32051

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 947-953 <STR>

R:Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.

Infect. Immun. 55, 1987-1996, 1987

A:Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1.

A:Reference number: S29515; MUID:87306837

A:Accession: S29516

A:Molecule type: DNA

A:Residues: 1-741, 'D', 743-953 <LOR>

A:Cross-references: EMBL:M20730; MUID:8150492; PIDN:AAA25529.1; PID:g150494

C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).

C:Genetics:

A:Gene: lktA

C:Function:

A:Description: lyses leukocytes

C:Superfamily: hemolysin A; hemolysin A homology

C:Keywords: calcium binding; cytotoxic; exotoxin; hemolysis; lipoprotein; tandem rep

F:238-784/Domain: hemolysin A homology <HIC>

F:716-807/Region: 9-residue repeats (G-X-G-[DN]-D-X-[LVYF]-X)

F:554/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 50.0%; Score 2325; DB 1; Length 953;

Best Local Similarity 49.9%; Pred. No. 1.6e-111;

Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps 13;

Oy 8 KSNIQAGLSTSGKLNLYLAIPKO--YDPQKGGTLNDFIKAADEGLARLAEENPHET 65

DB 28 QSTQAG-SLTKGAKKILYIPQYDTQGNGLQDLVKAEEGLGVQREERNRIAT 86

Oy 66 AKRSVDVNOFLSTOTGTATSAITKLEKFLQKHNKLKGLDSVENIDKRLKASNYLS 125

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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:58:48 ; Search time 75:59 seconds
(without alignments)
20,572 Million cell updates/sec

Title: US-09-884-696-13
Perfect score: 77
Sequence: 1 FNDIFHSGEGDLL 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
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20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	927	22	AA62110 M. bovis Dalton 2d
2	58	75.3	1049	18	AAW22159 ApxIIIB protein.
3	58	75.3	1049	21	AA51412 A. pleuropneumonia
4	58	75.3	1244	15	AA54781 Leukotoxin AppIIIA
5	52	67.5	758	17	AA86998 Enterohaemorrhagic
6	49	63.6	127	16	AA876990 Actinobacillus ant
7	49	63.6	450	22	AAE04637 Pasteurella haemol
8	49	63.6	608	22	AAE04636 Pasteurella haemol
9	49	63.6	924	12	AA10889 Leukotoxin 352 enc
10	49	63.6	924	14	AA42385 Recombinant leukot
11	49	63.6	924	14	AA42380 Recombinant leukot

12	49	63.6	924	14	AA42378 Recombinant leukot
13	49	63.6	926	12	AA14482 LKT352. Pasteurel
14	49	63.6	926	14	AA34545 Leukotoxin 352 pro
15	49	63.6	926	15	AA50291 Recombinant leukot
16	49	63.6	926	17	AAW03945 P. haemolytica tru
17	49	63.6	926	19	AAW79568 Leukotoxin 352 pol
18	49	63.6	936	14	AA34547 GNRH-leukotoxin ge
19	49	63.6	943	14	AA34546 Somatostatin-leuko
20	49	63.6	951	11	AA34548 Rotavirus VP4-leuk
21	49	63.6	953	11	AAW07167 105kd PFX protein
22	49	63.6	953	12	AA15159 Leukotoxin from P.
23	49	63.6	953	14	AA43865 Leukotoxin protein
24	49	63.6	953	15	AA60072 PtxA protein of Pa
25	49	63.6	953	22	AAE04638 Pasteurella haemol
26	49	63.6	977	17	AAW03942 LKT-GNRH protein f
27	49	63.6	977	19	AAW79569 LKT-GNRH chimeric
28	49	63.6	1022	18	AAW22152 ApxIA protein. AC
29	49	63.6	1022	21	AA51406 A. pleuropneumonia
30	49	63.6	1023	16	AAW76991 LhaA (low homology
31	49	63.6	1069	15	AA52748 Bovine IFNgamma/LK
32	49	63.6	1069	18	AAW13867 Chimeric protein #
33	49	63.6	1069	21	AAW21074 Bovine gamma-IFN/P
34	49	63.6	1098	13	AA22103 Bovine IL-2 - LKT
35	49	63.6	1098	15	AA52747 Bovine IL-2/LKT ch
36	49	63.6	1098	18	AAW13866 Chimeric protein #
37	49	63.6	1098	21	AAW21073 Bovine IL-2/Pasteu
38	46	59.7	956	12	AAW12561 APPA haemolysin an
39	46	59.7	956	18	AAW22156 ApxIIC protein. A
40	46	59.7	956	21	AA51410 A. pleuropneumonia
41	45	58.4	934	17	AAW7637 P. suis leukotoxin
42	42	54.5	138	18	AAW2740 Pseudomonas fluore
43	42	54.5	166	22	AAU37416 Staphylococcus aur
44	42	54.5	218	8	AAW70435 Haemolysin C-termi
45	42	54.5	276	22	AAU34347 Staphylococcus aur

ALIGNMENTS

RESULT 1
AAB62110 ID AAB62110 standard; Protein; 927 AA.
XX AC AAB62110;
XX 29-MAY-2001 (first entry)
XX M. bovis Dalton 2d RTX toxin A subunit.
XX Moraxella; antigen; immune response; infection; RTX toxin; vaccine;
XX Moraxella; antibacterial; A subunit.
XX Moraxella bovis.
XX WO200116172-AL.
XX 08-MAR-2001.
XX 31-AUG-2000; 2000WO-AU01048.
XX 31-AUG-1999; 99AU-0002571.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (UYME) UNIV MELBOURNE.
XX Farn J, Strugnell R, Tennent J;
XX WPI: 2001-235092/24.
XX N-PSDB; AA57290.
XX Novel Moraxella bovis antigen useful in compositions for raising immune
XX PT response in an animal, has protease, lipase or hemolysin activity
XX